

=====

Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: MSpencer

Timestamp: Mon May 07 12:02:37 EDT 2007

=====

Application No: 10573245 Version No: 1.0

Input Set:

Output Set:

Started: 2007-04-20 12:00:24.452
Finished: 2007-04-20 12:00:24.973
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 521 ms
Total Warnings: 1
Total Errors: 1
No. of SeqIDs Defined: 24
Actual SeqID Count: 24

ErrCode **Error Description**

E 320 Wrong Nucleic Acid Designator, gab in SEQID (5)
W 213 Artificial or Unknown found in <213> in SEQ ID (8)

SEQUENCE LISTING

<110> The University of York

<120> Expansion Polypeptides

<130> 2902076.1

<140> 10573245

<141> 2007-05-07

<150> 10/573,245

<151> 2006-03-23

<150> PCT/GB04/04058

<151> 2004-08-23

<160> 24

<170> PatentIn version 3.4

<210> 1

<211> 783

<212> DNA

<213> Craterostigma plantagineum

<220>

<221> CDS

<222> (1)..(783)

<400> 1

atg gcg ttt ctg ggc cgc att att att ttt gcg acc ttt ctg gcg att 48
Met Ala Phe Leu Gly Arg Ile Ile Ile Phe Ala Thr Phe Leu Ala Ile
1 5 10 15

acc agc agc agc cat ttt gcg cgc gcg tat tat ggc ggc gat ggc ggc 96
Thr Ser Ser Ser His Phe Ala Arg Ala Tyr Tyr Gly Gly Asp Gly Gly
20 25 30

tgg acc gat gcg cat gcg acc ttt tat ggc ggc agc gat gcg agc ggc 144
Trp Thr Asp Ala His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly
35 40 45

acc atg ggc ggc gcg tgc ggc tat ggc aac ctg tat agc cag ggc tat 192
Thr Met Gly Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr
50 55 60

ggc acc aac acc gcg gcg ctg agc acc gcg ctg ttt aac aac ggc ctg 240
Gly Thr Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu
65 70 75 80

agc tgc ggc agc tgc ttt gaa att aaa tgc gcg agc agc att agc ggc 288
Ser Cys Gly Ser Cys Phe Glu Ile Lys Cys Ala Ser Ser Ile Ser Gly
85 90 95

ggc ggc aaa tgg tgc ctg ccg ggc ggc agc att acc gtg acc gcg acc	336		
Gly Gly Lys Trp Cys Leu Pro Gly Gly Ser Ile Thr Val Thr Ala Thr			
100	105	110	
aac ttt tgc ccg ccg aac aac gcg ctg ccg aac aac gcg ggc ggc tgg	384		
Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn Asn Ala Gly Gly Trp			
115	120	125	
tgc aac ccg ccg ctg cag cat ttt gat ctg agc cag ccg gtg ttt cag	432		
Cys Asn Pro Pro Leu Gln His Phe Asp Leu Ser Gln Pro Val Phe Gln			
130	135	140	
cat att gcg cag tat cgc gcg ggc att gtg ccg gtg agc tat cgc cgc	480		
His Ile Ala Gln Tyr Arg Ala Gly Ile Val Pro Val Ser Tyr Arg Arg			
145	150	155	160
gtg ccg tgc cgc cgc ggc ggc att cgc ttt acc att aac ggc cat	528		
Val Pro Cys Arg Arg Gly Gly Ile Arg Phe Thr Ile Asn Gly His			
165	170	175	
agc tat ttt aac ctg gtg ctg att acc aac gtg ggc ggc ggc gat	576		
Ser Tyr Phe Asn Leu Val Leu Ile Thr Asn Val Gly Gly Ala Gly Asp			
180	185	190	
gtg cat gcg gtg agc att aaa ggc gcg acc acc gat tgg cag ccg atg	624		
Val His Ala Val Ser Ile Lys Gly Ala Thr Thr Asp Trp Gln Pro Met			
195	200	205	
agc cgc aac tgg ggc cag aac tgg cag agc aac gcg aac ccg aac ggc	672		
Ser Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn Ala Asn Pro Asn Gly			
210	215	220	
cag cgc ctg agc ttt aaa gtg acc acc agc gat ggc cgc acc ctg gtg	720		
Gln Arg Leu Ser Phe Lys Val Thr Thr Ser Asp Gly Arg Thr Leu Val			
225	230	235	240
agc aac aac gtg gcg ccg ccg aac tgg agc ttt ggc cag acc ttt gcg	768		
Ser Asn Asn Val Ala Pro Pro Asn Trp Ser Phe Gly Gln Thr Phe Ala			
245	250	255	
ggc gcg cag ttt aac	783		
Gly Ala Gln Phe Asn			
260			

<210> 2
<211> 261
<212> PRT
<213> Craterostigma plantagineum

<400> 2

Met Ala Phe Leu Gly Arg Ile Ile Phe Ala Thr Phe Leu Ala Ile			
1	5	10	15

Thr Ser Ser Ser His Phe Ala Arg Ala Tyr Tyr Gly Gly Asp Gly Gly

20

25

30

Trp Thr Asp Ala His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly
35 40 45

Thr Met Gly Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr
50 55 60

Gly Thr Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu
65 70 75 80

Ser Cys Gly Ser Cys Phe Glu Ile Lys Cys Ala Ser Ser Ile Ser Gly
85 90 95

Gly Gly Lys Trp Cys Leu Pro Gly Gly Ser Ile Thr Val Thr Ala Thr
100 105 110

Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn Asn Ala Gly Gly Trp
115 120 125

Cys Asn Pro Pro Leu Gln His Phe Asp Leu Ser Gln Pro Val Phe Gln
130 135 140

His Ile Ala Gln Tyr Arg Ala Gly Ile Val Pro Val Ser Tyr Arg Arg
145 150 155 160

Val Pro Cys Arg Arg Gly Gly Ile Arg Phe Thr Ile Asn Gly His
165 170 175

Ser Tyr Phe Asn Leu Val Leu Ile Thr Asn Val Gly Gly Ala Gly Asp
180 185 190

Val His Ala Val Ser Ile Lys Gly Ala Thr Thr Asp Trp Gln Pro Met
195 200 205

Ser Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn Ala Asn Pro Asn Gly
210 215 220

Gln Arg Leu Ser Phe Lys Val Thr Thr Ser Asp Gly Arg Thr Leu Val
225 230 235 240

Ser Asn Asn Val Ala Pro Pro Asn Trp Ser Phe Gly Gln Thr Phe Ala
245 250 255

Gly Ala Gln Phe Asn

260

<210> 3

<211> 657

<212> DNA

<213> Craterostigma plantagineum

<220>

<221> CDS

<222> (1)..(657)

<400> 3

gct acc ttt tat ggc ggc ggc gat gct agc ggc acc atg ggc ggc gct 48
Ala Thr Phe Tyr Gly Gly Asp Ala Ser Gly Thr Met Gly Gly Ala
1 5 10 15

tgc ggc tat ggc aac ctg tat agc acc ggc tat ggc acc aac acc gct 96
Cys Gly Tyr Gly Asn Leu Tyr Ser Thr Gly Tyr Gly Thr Asn Thr Ala
20 25 30

gct ctg agc acc gct ctg ttt aac aac ggc ctg acc tgc ggc gct tgc 144
Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Thr Cys Gly Ala Cys
35 40 45

tat gaa ctg acc tgc aac aac gat ccg cgc ggc tgg tgc ctg agc gct 192
Tyr Glu Leu Thr Cys Asn Asn Asp Pro Arg Gly Trp Cys Leu Ser Gly
50 55 60

acc att atg gtg acc gct acc aac ttt tgc ccg ccg aac ccg agc ctg 240
Thr Ile Met Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Pro Ser Leu
65 70 75 80

ccg aac gat aac ggc ggc tgg tgc aac ccg ccg cgc cag cat ttt gat 288
Pro Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg Gln His Phe Asp
85 90 95

ctg gct gaa ccg gct ttt ctg cag att gct cag tat aaa gct ggc att 336
Leu Ala Glu Pro Ala Phe Leu Gln Ile Ala Gln Tyr Lys Ala Gly Ile
100 105 110

gtg ccg gtg aac tat cgc cgc gtg ccg tgc cag aaa aaa ggc ggc att 384
Val Pro Val Asn Tyr Arg Arg Val Pro Cys Gln Lys Lys Gly Gly Ile
115 120 125

cgc ttt acc att aac ggc cat agc ttt ttt aac ctg gtg ctg gtg acc 432
Arg Phe Thr Ile Asn Gly His Ser Phe Phe Asn Leu Val Leu Val Thr
130 135 140

aac gtg ggc ggc gtg ggc gat gtg cat agc gtg agc att aaa ggc agc 480
Asn Val Gly Gly Val Gly Asp Val His Ser Val Ser Ile Lys Gly Ser
145 150 155 160

aac	ggc	ggc	tgg	cag	ccg	ctg	agc	cgc	aac	tgg	ggc	cag	aac	tgg	cag		528	
Asn	Gly	Gly	Trp	Gln	Pro	Leu	Ser	Arg	Asn	Trp	Gly	Gln	Asn	Trp	Gln			
																165	170	175
agc	aac	agc	tat	ctg	aac	ggc	cag	agc	ctg	agc	ttt	cag	gtg	acc	acc		576	
Ser	Asn	Ser	Tyr	Leu	Asn	Gly	Gln	Ser	Leu	Ser	Phe	Gln	Val	Thr	Thr			
																180	185	190
agc	gat	ggc	cgc	acc	gtg	acc	agc	tat	gat	gtg	gcg	ccg	cgc	ggc	tgg		624	
Ser	Asp	Gly	Arg	Thr	Val	Thr	Ser	Tyr	Asp	Val	Ala	Pro	Arg	Gly	Trp			
																195	200	205
cag	ttt	ggc	cag	acc	ttt	gaa	ggc	ggc	cag	ttt							657	
Gln	Phe	Gly	Gln	Thr	Phe	Glu	Gly	Gly	Gln	Phe								
																210	215	
<210>	4																	
<211>	219																	
<212>	PRT																	
<213>	Craterostigma	plantagineum																
<400>	4																	
Ala	Thr	Phe	Tyr	Gly	Gly	Gly	Asp	Ala	Ser	Gly	Thr	Met	Gly	Gly	Ala			
1																15		
Cys	Gly	Tyr	Gly	Asn	Leu	Tyr	Ser	Thr	Gly	Tyr	Gly	Thr	Asn	Thr	Ala			
																20	25	30
Ala	Leu	Ser	Thr	Ala	Leu	Phe	Asn	Asn	Gly	Leu	Thr	Cys	Gly	Ala	Cys			
																35	40	45
Tyr	Glu	Leu	Thr	Cys	Asn	Asn	Asp	Pro	Arg	Gly	Trp	Cys	Leu	Ser	Gly			
																50	55	60
Thr	Ile	Met	Val	Thr	Ala	Thr	Asn	Phe	Cys	Pro	Pro	Asn	Pro	Ser	Leu			
																65	70	75
Pro	Asn	Asp	Asn	Gly	Gly	Trp	Cys	Asn	Pro	Pro	Arg	Gln	His	Phe	Asp			
																85	90	95
Leu	Ala	Glu	Pro	Ala	Phe	Leu	Gln	Ile	Ala	Gln	Tyr	Lys	Ala	Gly	Ile			
																100	105	110
Val	Pro	Val	Asn	Tyr	Arg	Arg	Val	Pro	Cys	Gln	Lys	Lys	Gly	Gly	Ile			
																115	120	125
Arg	Phe	Thr	Ile	Asn	Gly	His	Ser	Phe	Phe	Asn	Leu	Val	Leu	Val	Thr			

130	135	140
Asn Val Gly Gly Val Gly Asp Val His Ser Val Ser Ile Lys Gly Ser		
145	150	155
160		
Asn Gly Gly Trp Gln Pro Leu Ser Arg Asn Trp Gly Gln Asn Trp Gln		
165	170	175
Ser Asn Ser Tyr Leu Asn Gly Gln Ser Leu Ser Phe Gln Val Thr Thr		
180	185	190
Ser Asp Gly Arg Thr Val Thr Ser Tyr Asp Val Ala Pro Arg Gly Trp		
195	200	205
Gln Phe Gly Gln Thr Phe Glu Gly Gly Gln Phe		
210	215	
<210> 5		
<211> 672		
<212> DNA		
<213> Craterostigma plantagineum		
<220>		
<221> CDS		
<222> (1)..(672)		
<400> 5		
tgc cat gcg acc ttt tat ggc ggc agc gat gcg agc ggc acc atg ggc 48		
Cys His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly		
1	5	10
		15
ggc gcg tgc ggc tat ggc aac ctg tat agc cag ggc tat ggc acc aac 96		
Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn		
20	25	30
acc gcg gcg ctg agc acc acc ctg ttt aac aac ggc ctg gcg tgc ggc 144		
Thr Ala Ala Leu Ser Thr Thr Leu Phe Asn Asn Gly Leu Ala Cys Gly		
35	40	45
agc tgc tat cag gtg cgc tgc gaa ggc ggc ccg aaa tgg tgc gtg cgc 192		
Ser Cys Tyr Gln Val Arg Cys Glu Gly Gly Pro Lys Trp Cys Val Arg		
50	55	60
ggc ggc gat cgc att att acc gtg acc gcg acc aac ttt tgc ccg ccg 240		
Gly Gly Asp Arg Ile Ile Thr Val Thr Ala Thr Asn Phe Cys Pro Pro		
65	70	75
		80
aac tat gcg ctg gcg aac gat aac ggc ggc tgg tgc aac ccg ccg cgc 288		
Asn Tyr Ala Leu Ala Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg		
85	90	95

cag cat ttt gat atg gcg cag ccg gcg ttt gtg cgc att gcg cat tat	336		
Gln His Phe Asp Met Ala Gln Pro Ala Phe Val Arg Ile Ala His Tyr			
100	105	110	
cgc gcg ggc att gtg ccg att agc tat cgc cgc gtg agc tgc gtg aaa	384		
Arg Ala Gly Ile Val Pro Ile Ser Tyr Arg Arg Val Ser Cys Val Lys			
115	120	125	
aaa ggc ggc att cgc ctg acc att aac ggc cat agc tat ttt aac ctg	432		
Lys Gly Gly Ile Arg Leu Thr Ile Asn Gly His Ser Tyr Phe Asn Leu			
130	135	140	
gtg ctg gtg agc aac gtg ggc ggc agc ggc gat gtg cat gcg gtg tgg	480		
Val Leu Val Ser Asn Val Gly Gly Ser Gly Asp Val His Ala Val Trp			
145	150	155	160
att aaa ggc agc ggc ggc ccg tgg cag gcg atg acc cgc aac tgg	528		
Ile Lys Gly Ser Gly Gly Pro Trp Gln Ala Met Thr Arg Asn Trp			
165	170	175	
ggc cag aac tgg cag agc aac agc tat ctg gat ggc cag agc ctg agc	576		
Gly Gln Asn Trp Gln Ser Asn Ser Tyr Leu Asp Gly Gln Ser Leu Ser			
180	185	190	
ttt att gtg cgc gcg ggc gat ggc cgc acc gtg acc gcg aac gab att	624		
Phe Ile Val Arg Ala Gly Asp Gly Arg Thr Val Thr Ala Asn Xaa Ile			
195	200	205	
gtg ccg cgc ggc tgg cag ttt ggc cag acc ttt gaa ggc ccg cag ttt	672		
Val Pro Arg Gly Trp Gln Phe Gly Gln Thr Phe Glu Gly Pro Gln Phe			
210	215	220	

<210> 6
<211> 224
<212> PRT
<213> Craterostigma plantagineum

<220>
<221> misc_feature
<222> (207)..(207)
<223> The 'Xaa' at location 207 stands for Glu, or Asp.

<400> 6

Cys His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly			
1	5	10	15

Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn		
20	25	30

Thr Ala Ala Leu Ser Thr Thr Leu Phe Asn Asn Gly Leu Ala Cys Gly		
35	40	45

Ser Cys Tyr Gln Val Arg Cys Glu Gly Gly Pro Lys Trp Cys Val Arg
50 55 60

Gly Gly Asp Arg Ile Ile Thr Val Thr Ala Thr Asn Phe Cys Pro Pro
65 70 75 80

Asn Tyr Ala Leu Ala Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg
85 90 95

Gln His Phe Asp Met Ala Gln Pro Ala Phe Val Arg Ile Ala His Tyr
100 105 110

Arg Ala Gly Ile Val Pro Ile Ser Tyr Arg Arg Val Ser Cys Val Lys
115 120 125

Lys Gly Gly Ile Arg Leu Thr Ile Asn Gly His Ser Tyr Phe Asn Leu
130 135 140

Val Leu Val Ser Asn Val Gly Gly Ser Gly Asp Val His Ala Val Trp
145 150 155 160

Ile Lys Gly Ser Gly Gly Pro Trp Gln Ala Met Thr Arg Asn Trp
165 170 175

Gly Gln Asn Trp Gln Ser Asn Ser Tyr Leu Asp Gly Gln Ser Leu Ser
180 185 190

Phe Ile Val Arg Ala Gly Asp Gly Arg Thr Val Thr Ala Asn Xaa Ile
195 200 205

Val Pro Arg Gly Trp Gln Phe Gly Gln Thr Phe Glu Gly Pro Gln Phe
210 215 220

<210> 7
<211> 8
<212> PRT
<213> Craterostigma plantagineum

<400> 7

Ala Ser Ser Ile Ser Gly Gly Gly
1 5

<210> 8

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerative primer

<220>
<221> misc_feature
<222> (2)..(2)
<223> s is Guanine or cytosine

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (6)..(6)
<223> y is pyrimidine

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (12)..(12)
<2